

SEQUENCE LISTING

<110> Barnett, Susan
Zur Megede, Jan

<120> POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF

<130> PP01631.101

<140>

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<150> 09/475,704

<151> 1999-12-30

<160> 45

<170> PatentIn Ver. 2.0

<210> 1

<211> 60

<212> DNA

<213> Human immunodeficiency virus

<400> 1

gacatcaagc agggccccaaggagcccttc cgcgactacg tggaccgctt cttcaagacc 60

<210> 2

<211> 60

<212> DNA

<213> Human immunodeficiency virus

<400> 2

gacatccgcc agggccccaaggagcccttc cgcgactacg tggaccgctt cttcaagacc 60

<210> 3

<211> 1479

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic Gag
of HIV strain AF110965

<400> 3

atgggcgccc gcgccagcat cctgcgcggc ggcaagctgg acgcctggga gcgcatccgc 60
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ctggagaagt tcgccctgaa ccccgccctg ctggagacca gcgagggctg caagcagatc 180
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gccgacaagg gcaagggtgag ccagaactac cccatcgtgc agaacctgca gggccagatg 420
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gccttcagcc ccgaggtgat ccccatgttc accgcctga gcgagggcgc cccccccag 540
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gacaccatca acgaggaggg cgccgagtg gaccgcgtgc acccctgca cgccggcccc 660
atcgcccccg gccagatgcg cgagccccgc ggcagcgaca tcgcccggcac caccagcacc 720
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aagcgggtgga tcatcctggg cctgaacaag atcgtgcgga tgtacagccc cgtgagcatc 840
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cccggcaact tcctgcagag ccgccccgag ccaccgccc ccccgccga gagcttccgc 1380
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<210> 4

<211> 1509

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic Gag
of HIV strain AF110967

<400> 4

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ctggagggct tcgcctgaa ccccgccctg ctggagaccg ccgagggtg caagcagatc 180
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ctggacaaga tcgaggagga gcagaacaag tcccagcaga agaccagca ggccaaggag 360
gccgacggca aggtgagcca gaactacccc atcgtgcaga acctgcaggg ccagatggtg 420
caccaggcca tcagcccccg caccctgaac gcctgggtga aggtgatcga ggagaaggcc 480
ttcagccccg aggtgatccc catgttcacc gccctgagcg agggcgccac ccccaggac 540
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cagaacgcca acccgactg caagaccatc ctgcgcgctc tcggcccccg cgccaccctg 1020
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tgccgcgccc ccgcaagaa gggctgctgg aagtgcggca aggagggcca ccagatgaag 1260
gactgcaccg agcggcaggc caacttcctg ggcaagatct ggcccagcca caagggccgc 1320
cccggcaact tcctgcagaa ccgagcgag ccccgccccc ccaccgtgc caccgcccc 1380
cccgcgaga gcttccgctt cgaggagacc acccccgccc ccaagcagga gcccaaggac 1440
cgcgagccct acccgagcc cctgaccgcc ctgcgcagcc tgttcggcag cgccccctg 1500
agccagtaa

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<210> 5
 <211> 141
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Env common
 region of HIV strain AF110968

<400> 5
 accatcacca tcacctgccg catcaagcag atcatcaaca tgtggcagaa ggtggggccgc 60
 gccatgtacg ccccccccat cgccggcaac ctgacctgcg agagcaacat caccggcctg 120
 ctgctgaccc gcgacggcgg c 141

<210> 6
 <211> 1431
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic
 gp120 coding region of HIV strain AF110968

<400> 6
 agcgtggtgg gcaacctgtg ggtgaccgtg tactacggcg tgcccgtgtg gaaggaggcc 60
 aagaccaccc tgttctgcac cagcgacgcc aaggcctacg agaccgaggt gcacaacgtg 120
 tggggcaccc acgcctgcgt gccaccgac cccaaccccc aggagatcgt gctggagaac 180
 gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
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 ctgaagtgcc gcaacgtgaa cgccaccaac aacatcaaca gcatgatcga caacagcaac 360
 aagggcgaga tgaagaactg cagcttcaac gtgaccaccg agctgcgcga ccgcaagcag 420
 gaggtgcacg ccctgttcta ccgcctggac gtggtgcccc tgcagggcaa caacagcaac 480
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 ttcgacccca tccccatcca ctactgcacc cccgccggct acgccatcct gaagtgcaac 600
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 aagcccgtga agatcgtgtg cgtgcgcccc aacaacaaca cccgcaagag cgtgcgcac 840
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 gccccccca tcgcccggcaa cctgacctgc gagagcaaca tcaccggcct gctgctgacc 1260
 cgcgacggcg gcaagaccgg ccccaacgac accgagatct tccgccccgg cggcgcgac 1320
 atgcgcgaca actggcgcaa cgagctgtac aagtacaagg tgggtggagat caagcccctg 1380
 ggcgtggccc ccaccgaggg caagcgccgc gtggtggagc gcgagaagcg c 1431

<210> 7
 <211> 1944
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
gp140 coding region of HIV strain AF110968

<400> 7

agcgtggtgg gcaacctgtg ggtgaccgtg tactacggcg tgcccgtgtg gaaggaggcc 60
aagaccaccc tgttctgcac cagcgacgcc aaggcctacg agaccgaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gccaccgac cccaaccccc aggagatcgt gctggagaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
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ctgaagtgcc gcaacgtgaa cgccaccaac aacatcaaca gcatgatcga caacagcaac 360
aagggcgaga tgaagaactg cagcttcaac gtgaccaccg agctgcgcga ccgcaagcag 420
gaggtgcacg ccctgttcta ccgcctggac gtggtgcccc tgcagggcaa caacagcaac 480
gagtaccgcc tgatcaactg caacaccagc gccatcacc aggcctgcc caaggtgagc 540
ttcgacccca tccccatcca ctactgcacc cccgcgggt acgccatcct gaagtgaac 600
aaccagacct tcaacggcac cgccccctgc aacaacgtga gcagcgtgca gtgcgcccac 660
ggcatcaagc ccgtggtgag caccagctg ctgctgaacg gcagcctggc caagggcgag 720
atcatcatcc gcagcgâgaa cctggccaac aacgccaaga tcatcatcgt gcagctgaac 780
aagcccgtga agatcgtgtg cgtgcgcccc aacaacaaca cccgcaagag cgtgcgcac 840
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agcaaccgca gccacgacga gatctgggac aacatgacct ggatgcagt ggaccgcgag 1800
atcaacaact acaccgacac catctaccgc ctgctggagg agagccagaa ccagcaggag 1860
aagaacgaga aggacctgct ggccctggac agctggcaga acctgtggaa ctggttcagc 1920
atcaccaact ggctgtggta catc 1944

<210> 8

<211> 2466

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
gp160 coding region of HIV strain AF110968

<400> 8

agcgtggtgg gcaacctgtg ggtgaccgtg tactacggcg tgcccgtgtg gaaggaggcc 60
aagaccaccc tgttctgcac cagcgacgcc aaggcctacg agaccgaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gccaccgac cccaaccccc aggagatcgt gctggagaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc tgcgtgaagc tgacccccct gtgctgacc 300


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agcagctgga gcaaccgcag ccacgacgag atctgggaca acatgacctg gatgcagtgg 360
gaccgcgaga tcaacaacta caccgacacc atctaccgcc tgctggagga gagccagaac 420
cagcaggaga agaacgagaa ggacctgctg gccctggaca gctggcagaa cctgtggaac 480
tggttcagca tcaccaactg gctgtggtac atcaagatct tcatcatgat cgtgggcggc 540
ctgatcgccc tgcgcatcat cttcgccgtg ctgagcatcg tgaaccgcgt gcgccagggc 600
tacagccccc tgcccttcca gacctgacc cccaaccccc gcgagcccca ccgcctgggc 660
cgcacgcagg aggagggcgg cgagcaggac cgcgcccgca gcatccgcct ggtgagcgcc 720
ttcctggccc tggcctggga cgacctgcgc agcctgtgcc tgttcagcta ccaccgcctg 780
cgcgacttca tctgatcgc cgcccgctg ctggagctgc tgggcccagc cggctgggag 840
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atcagcctgc tggacacat cgccatcgcc gtggccgagg gcaccgaccg catcatcgag 960
ttcatccagc gcatctgccg cgccatccgc aacatcccc gccgcatccg ccagggcttc 1020
gaggccgccc tgcag                                     1035

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<210> 11

<211> 144

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic Env
common region of HIV strain AF110975

<400> 11

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agcatcatca ccctgccctg ccgcatcaag cagatcatcg acatgtggca gaaggtgggc 60
cgcgccatct acgccccccc catcgagggc aacatcacct gcagcagcag catcaccggc 120
ctgctgctgg ccgcgcagcg cggc                                     144

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<210> 12

<211> 1437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
gp120 coding region of HIV strain AF110975

<400> 12

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agcggcctgg gcaacctgtg ggtgaccgtg tacgacggcg tgcccgtgtg gcgcgaggcc 60
agcaccaccc tgttctgcgc cagcgacgcc aaggcctacg agaaggaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gcccaccgac cccaaccccc aggagatcga gctggacaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc cgcgtaagc tgacccccct gtgcgtgacc 300
ctgaagtgca ccaactacag caccaactac agcaaaccca tgaacgccac cagctacaac 360
aacaacacca ccgaggagat caagaactgc accttcaaca tgaccaccga gctgcgcgac 420
aagaagcagc aggtgtacgc cctgttctac aagctggaca tcgtgcccct gaacagcaac 480
agcagcgagt accgcctgat caactgcaac accagcgcca tcaccaggc ctgccccaaag 540
gtgagcttcg accccatccc catccactac tgcgcccccg ccggctacgc catcctgaag 600
tgcaagaaca acaccagcaa cggcaccggc ccctgccaga acgtgagcac cgtgcagtgc 660
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cactgaacg acagcgtgga gatcgtgtgc acccgcccca acaacaacac ccgcaagggc 840
atccgcatcg gccccggcca gaccttctac gccaccgaga acatcatcgg cgacatccgc 900
caggccact gcaacatcag cgccggcgag tggaacaagg ccgtgcagcg cgtgagcgcc 960

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aagctgcgcg agcaacttccc caacaagacc atcgagttcc agcccagcag cggcggcgac 1020
ctggagatca ccacccacag cttcaactgc cgcggcgagt tcttctactg caacaccagc 1080
aagctgttca acagcagcta caacggcacc agctaccgcg gcaccgagag caacagcagc 1140
atcatcaccg tgccctgccc catcaagcag atcatcgaca tgtggcagaa ggtggggccgc 1200
gccatctacg ccccccccat cgaggggaac atcacctgca gcagcagcat caccggcctg 1260
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ggcgacatga aggacaactg gcgcaacgag ctgtacaagt acaaggtggt ggagatcaag 1380
cccctgggcg tggccccccac cgaggccaag cgccgcgtgg tggagcgcca gaagcgc 1437

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<210> 13

<211> 1950

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
gp140 coding region of HIV strain AF110975

<400> 13

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tggggcaccg acgctgctgt gccaccgac cccaaccccc aggagatcga gctggacaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
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aacaacacca ccgaggagat caagaactgc accttcaaca tgaccaccga gctgcgcgac 420
aagaagcagc aggtgtacgc cctgttctac aagctggaca tcgtgcccct gaacagcaac 480
agcagcgagt accgcctgat caactgcaac accagcgcca tcaccaggc ctgccccagg 540
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tgcaagaaca acaccagcaa cggcaccggc ccctgccaga acgtgagcac cgtgcagtcg 660
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aaggagatca gcaactacac cggcatcatc taccgcctgc tggaggagag ccagaaccag 1860
caggagcaga acgagaagga cctgctggcc ctggacagcc gcaacaacct gtggagctgg 1920
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<210> 14

<211> 2493
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic
 gp160 coding region of HIV strain AF110975

<400> 14
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 agcaccaccc tgttctgcgc cagcgacgcc aaggcctacg agaaggaggt gcacaacgtg 120
 tgggccaccc acgcctgcgt gccaccgac cccaaccccc aggagatcga gctggacaac 180
 gtgaccgaga acttcaacat gtggaagaac gacatggttg accagatgca cgaggacatc 240
 atcagcctgt gggaccagag cctgaagccc cgcgtgaagc tgacccccct gtgcgtgacc 300
 ctgaagtgca ccaactacag caccaactac agcaacacca tgaacgccac cagctacaac 360
 aacaacacca ccgaggagat caagaactgc accttcaaca tgaccaccga gctgcgcgac 420
 aagaagcagc aggtgtacgc cctgttctac aagctggaca tcgtgcccct gaacagcaac 480
 agcagcgagt accgcctgat caactgcaac accagcgcca tcaccaggc ctgccccaaag 540
 gtgagcttcg accccatccc catccactac tgcccccgcg ccggtacgc catcctgaag 600
 tgcaagaaca acaccagcaa cggcaccggc ccctgccaga acgtgagcac cgtgcagtgc 660
 acccacggca tcaagcccgt ggtgagcacc cccctgctgc tgaacggcag cctggccgag 720
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 cccctggcgg tggccccac cgaggccaag cgcgcgtgg tggagcgcga gaagcgcgcc 1440
 gtgggcatcg gcgcctgat ctctggcttc ctgggcgcgc ccggcagcaa catgggcgcc 1500
 gccagcatca ccctgaccgc ccaggcccgc cagctgctga gcggcatcgt gcagcagcag 1560
 agcaacctgc tgcgcgccat cgaggcccag cagcacatgc tgcagctgac cgtgtggggc 1620
 atcaagcagc tgcaggcccg cgtgctggcc atcgagcgct acctgaagga ccagcagctg 1680
 ctgggcatct ggggctgcag cggcaagctg atctgcacca ccaccgtgcc ctggaacagc 1740
 agctggagca acaagacca gggcgagatc tgggagaaca tgacctgat gcagtgggac 1800
 aaggagatca gcaactacac cggcatcatc taccgcctgc tggaggagag ccagaaccag 1860
 caggagcaga acgagaagga cctgctggcc ctggacagcc gcaacaacct gtggagctgg 1920
 ttcaacatca gcaactggct gtggtacatc aagatcttca tcatgatcgt gggcggcctg 1980
 atcggcctgc gcatcatctt cgcctgctg agcatcgtga accgcgtgcg ccagggtac 2040
 agccccctga gcttccagac cctgaccccc aacccccgcg gcctggaccg cctgggccgc 2100
 atcaggagg agggcggcga gcaggaccgc gaccgcagca tccgcctggt gcagggttc 2160
 ctggccctgg cctgggacga cctgcgcagc ctgtgcctgt tcagctacca ccgcctgcgc 2220
 gacctgatcc tggtagccgc ccgcgtggtg gagctgctgg gccgcagcag cccccgcggc 2280
 ctgcagcgcg gctgggaggc cctgaagtac ctgggcagcc tggtagcagta ctggggcctg 2340
 gagctgaaga agagcggcac cagcctgctg gacagcatcg ccacgcgcgt ggccgagggc 2400
 accgaccgca tcatcgaggt gatccagcgc atctaccgcg ccttctgcaa catccccgcg 2460
 cgcgtgcgcc agggcttcga ggccgcctg cag 2493

<210> 15
 <211> 2565

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
signal sequence and gp160 coding region of HIV
strain AF110975

<400> 15

```
atgcgcgtgc gcggcacccct gcgcagctgg cagcagtggt ggatctgggg catcctgggg 60
ttctggatct gcagcggcct gggcaacctg tgggtgaccg tgtacgacgg cgtgcccgtg 120
tggcgcgagg ccagcaccac cctgttctgc gccagcgaag ccaaggccta cgagaaggag 180
gtgcacaacg tgtgggccac ccacgcctgc gtgcccaccg accccaaccc ccaggagatc 240
gagctggaca acgtgaccga gaacttcaac atgtggaaga acgacatggt ggaccagatg 300
cacgaggaca tcatcagcct gtgggaccag agcctgaagc cccgcgtgaa gctgaccccc 360
ctgtgcgtga ccctgaagtgc caccaactac agcaccaact acagcaaacac catgaacgcc 420
accagctaca acaacaacac caccgaggag atcaagaact gcaccttcaa catgaccacc 480
gagctgcgcg acaagaagca gcagggtgtac gccctgttct acaagctgga catcgtgccc 540
ctgaacagca acagcagcga gtaccgcctg atcaactgca acaccagcgc catcaccagc 600
gcctgcccca aggtgagctt cgaccccatc cccatccact actgcgcccc cgccggctac 660
gccatcctga agtgcaagaa caacaccagc aacggcaccg gccctgcca gaacgtgagc 720
accgtgcagt gcacccacgg catcaagccc gtggtgagca cccccctgct gctgaacggc 780
agcctggccg agggcggcga gatcatcatc cgcagcaaga acctgagcaa caacgcctac 840
accatcatcg tgcacctgaa cgacagcgtg gagatcgtgt gcacccgccc caacaacaac 900
accgcgaagg gcatccgcat cggccccggc cagaccttct acgccaccga gaacatcatc 960
ggcgacatcc gccaggccca ctgcaacatc agcgccggcg agtggaacaa ggccgtgcag 1020
cgcgtagcgc ccaagctgcg cgagcacttc cccaacaaga ccacgagtt ccagcccagc 1080
agcggcggcg acctggagat caccacccac agcttcaact gccgcggcga gttcttctac 1140
tgcaacacca gcaagctggt caacagcagc tacaacggca ccagctaccg cggcaccgag 1200
agcaacagca gcatcatcac cctgccctgc cgcacaaagc agatcatcga catgtggcag 1260
aagggtgggg ccgcacatcta cccccccccc atcgagggca acatcacctg cagcagcagc 1320
atcacccggc tgctgctggc ccgcgacggc ggcctggaca acatcaccac cgagatcttc 1380
cgcccccagg gcggcgacat gaaggacaac tggcgcaacg agctgtacaa gtacaagggtg 1440
gtggagatca agccccctgg cgtggccccc accgaggcca agcgcccgct ggtggagcgc 1500
gagaagcgcg ccgtgggcat cggcgccgtg atcttcggct tcctgggccc cgccggcagc 1560
aacatgggcg ccgccagcat caccctgacc gccaggccc gccagctgct gagcggcatc 1620
gtgcagcagc agagcaacct gctgcgcgcc atcgaggccc agcagcacat gctgcagctg 1680
accgtgtggg gcatcaagca gctgcaggcc cgcgctgctg ccacgagcgc ctacctgaag 1740
gaccagcagc tgctgggcat ctggggctgc agcggcaagc tgatctgcac caccaccgtg 1800
ccctggaaca gcagctggag caacaagacc cagggcgaga tctgggagaa catgacctgg 1860
atgcagtggg acaaggagat cagcaactac accggcatca tctaccgcct gctggaggag 1920
agccagaacc agcaggagca gaacgagaag gacctgctgg ccctggacag ccgcaacaac 1980
ctgtggagct gggttcaacat cagcaactgg ctgtggtaca tcaagatctt catcatgatc 2040
gtggggcgcc tgatcggcct gcgcacatc ttcgcctgct tgagcatcgt gaaccgcgtg 2100
cgccagggtt acagccccct gagcttccag accctgacct ccaacccccg cggcctggag 2160
cgctggggc gcatcgagga ggaggcgcc gagcaggacc gcgaccgcag catccgctg 2220
gtgcagggtt tcctggccct ggccctgggac gacctgcgca gcctgtgcct gttcagctac 2280
caccgcctgc gcgacctgat cctggtgacc gcccgcgtgg tggagctgct gggccgcagc 2340
agcccccgcg gcctgcagcg cggctgggag gccctgaagt acctgggcag cctggtgcag 2400
tactggggcc tggagctgaa gaagagcgcc accagcctgc tggacagcat cgccatcgcc 2460
gtggccgagg gcaccgaccg catcatcgag gtgatccagc gcactaccg cgccctctgc 2520
aacatcccc gccgcgtgcg ccagggttcc gaggccgccc tgcag 2565
```

<210> 16

<211> 1056
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic a
 gp41 coding region of HIV strain AF110975

<400> 16
 gccgtgggca tcggcgccgt gatcttcggc ttcctgggcg ccgcccgcag caacatgggc 60
 gccgccagca tcaccctgac cgcccaggcc cgccagctgc tgagcggcat cgtgcagcag 120
 cagagcaacc tgctgcgcgc catcgaggcc cagcagcaca tgctgcagct gaccgtgtgg 180
 ggcataaagc agctgcaggc ccgcgtgctg gccatcgagc gctacctgaa ggaccagcag 240
 ctgctgggca tctggggctg cagcggcaag ctgatctgca ccaccaccgt gccctggaac 300
 agcagctgga gcaacaagac ccagggcgag atctgggaga acatgacctg gatgcagtgg 360
 gacaaggaga tcagcaacta caccggcatc atctaccgcc tgctggagga gagccagaac 420
 cagcaggagc agaacgagaa ggacctgctg gccctggaca gccgcaacaa cctgtggagc 480
 tggttcaaca tcagcaactg gctgtggtac atcaagatct tcatcatgat cgtgggcggc 540
 ctgatcggcc tgcgcacatc cttcgccgtg ctgagcatcg tgaaccgcgt gcgccagggc 600
 tacagccccc tgagcttcca gacctgacc cccaaccccc gcggcctgga ccgcctgggc 660
 cgcacagagg aggagggcgg cgagcaggac cgcgaccgca gcatccgcct ggtgcagggc 720
 ttcctggccc tggcctggga cgacctgcgc agcctgtgcc tggtcagcta ccaccgctg 780
 cgcgacctga tcttgggtgac cgcccgctg gtggagctgc tgggccgcag cagccccgcg 840
 ggctgcagc gcggctggga ggcctgaag tacctgggca gcctggtgca gtactggggc 900
 ctggagctga agaagagcgc caccagcctg ctggacagca tcgccatcgc cgtggccgag 960
 ggcaccgacc gcatcatcga ggtgatccag cgcactacc gcgccttctg caacatcccc 1020
 cgccgcgtgc gccagggctt cgaggccgcc ctgcag 1056

<210> 17
 <211> 492
 <212> PRT
 <213> Human immunodeficiency virus

<400> 17
 Met Gly Ala Arg Ala Ser Ile Leu Arg Gly Gly Lys Leu Asp Ala Trp
 1 5 10 15
 Glu Arg Ile Arg Leu Arg Pro Gly Gly Lys Lys Cys Tyr Met Met Lys
 20 25 30
 His Leu Val Trp Ala Ser Arg Glu Leu Glu Lys Phe Ala Leu Asn Pro
 35 40 45
 Gly Leu Leu Glu Thr Ser Glu Gly Cys Lys Gln Ile Ile Arg Gln Leu
 50 55 60
 His Pro Ala Leu Gln Thr Gly Ser Glu Glu Leu Lys Ser Leu Phe Asn
 65 70 75 80
 Thr Val Ala Thr Leu Tyr Cys Val His Glu Lys Ile Glu Val Arg Asp
 85 90 95
 Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Cys Gln
 100 105 110

005040-EEFESB

Gln Lys Ile Gln Gln Ala Glu Ala Ala Asp Lys Gly Lys Val Ser Gln	115	120	125
Asn Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala	130	135	140
Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu Lys	145	150	155 160
Ala Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu Gly	165	170	175
Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His	180	185	190
Gln Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala	195	200	205
Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly	210	215	220
Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr	225	230	235 240
Leu Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Ile Pro Val	245	250	255
Gly Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val	260	265	270
Arg Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Lys Gln Gly Pro Lys	275	280	285
Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Phe Lys Thr Leu Arg Ala	290	295	300
Glu Gln Ser Thr Gln Glu Val Lys Asn Trp Met Thr Asp Thr Leu Leu	305	310	315 320
Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Arg Ala Leu Gly	325	330	335
Pro Gly Ala Ser Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly	340	345	350
Gly Pro Ser His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Ala	355	360	365
Asn Thr Ser Val Met Met Gln Lys Ser Asn Phe Lys Gly Pro Arg Arg	370	375	380
Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Arg Asn	385	390	395 400

Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
405 410 415

His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
420 425 430

Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Ser Arg
435 440 445

Pro Glu Pro Thr Ala Pro Pro Ala Glu Ser Phe Arg Phe Glu Glu Thr
450 455 460

Thr Pro Gly Gln Lys Gln Glu Ser Lys Asp Arg Glu Thr Leu Thr Ser
465 470 475 480

Leu Lys Ser Leu Phe Gly Asn Asp Pro Leu Ser Gln
485 490

<210> 18
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
signal sequence of HIV strain AF110968

<400> 18
atgcgcgtga tgggcatact gaagaactac cagcagtggt ggatgtgggg catcctgggc 60
ttctggatgc tgatcatcag c 81

<210> 19
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
signal sequence of HIV strain AF110975

<400> 19
atgcgcgtgc gcggcatact gcgcagctgg cagcagtggt ggatctgggg catcctgggc 60
ttctggatct gc 72

<210> 20
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic Gag
coding sequence of HIV strain AF110965

<400> 20

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atgggcgccc gcgccagcat cctgcgcggc ggcaagctgg acgcctggga gcgcatccgc 60
ctgcgccccg gcggcaagaa gtgctacatg atgaagcacc tgggtgtggc cagccgcgag 120
ctggagaagt tcgccctgaa ccccgccctg ctggagacca gcgagggtg caagcagatc 180
atccgccagc tgcaccccg cctgcagacc ggcagcgagg agctgaagag cctgttcaac 240
accgtggcca cctgtactg cgtgcacgag aagatcgagg tgcgcgacac caaggaggcc 300
ctggacaaga tcgaggagga gcagaacaag tgccagcaga agatccagca ggccgaggcc 360
gccgacaagg gcaaggtgag ccagaactac cccatcgtgc agaacctgca gggccagatg 420
gtgcaccagg ccatcagccc ccgcacctg aacgcctggg tgaaggtgat cgaggagaag 480
gccttcagcc ccgaggtgat ccccatgttc accgcctga gcgaggggcg cccccccag 540
gacctgaaca ccatgctgaa caccgtgggc ggccaccagg ccgccatgca gatgctgaag 600
gacaccatca acgaggaggc cgccgagtgg gaccgctgc acccctgca cgccggcccc 660
atcgcccccg gccagatgcg cgagccccgc ggcagcgaca tcgccggcac caccagcacc 720
ctgcaggagc agatcgccctg gatgaccagc aacccccca tccccgtggg cgacatctac 780
aagcgctgga tcctcctggg cctgaacaag atcgtgcgca tgtacagccc cgtgagcatc 840
ctggacatca agcagggccc caaggagccc ttccgcgact acgtggaccg cttcttcaag 900
accctgcgcg ccgagcagag caccagggag gtgaagaact ggatgaccga caccctgctg 960
gtgcagaacg ccaaccccg ctgcaagacc atcctgcgcg ccctggggcc cgccgcagc 1020
ctggaggaga tgatgaccgc ctgccagggc gtgggcggcc ccagccaca ggcccgctg 1080
ctggccgagg ccatgagcca ggccaacacc agcgtgatga tgcagaagag caacttcaag 1140
ggcccccgcc gcctcgtgaa gtgcttcaac tgcggcaagg agggccacat cgcccgcaac 1200
tgccgcgccc ccgcaagaa gggctgctgg aagtgcggca aggagggcca ccagatgaag 1260
gactgcaccg agcgcacggc caacttctg ggcaagatct ggccagcca caaggccgc 1320
cccggcaact tcctgcagag ccgccccgag cccaccgccc ccccgccga gagcttccgc 1380
ttcgaggaga ccacccccg ccagaagcag gagagcaagg accgcgagac cctgaccagc 1440
ctgaagagcc tgttcggcaa cgacccccctg agccagtaa 1479

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<210> 21

<211> 1509

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic Gag coding sequence of HIV strain AF110967

<400> 21

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atgggcgccc gcgccagcat cctgcgcggc gagaagctgg acaagtggga gaagatccgc 60
ctgcgccccg gcggcaagaa gcactacatg ctgaagcacc tgggtgtggc cagccgcgag 120
ctggagggtt tcgccctgaa ccccgccctg ctggagaccg ccgagggtg caagcagatc 180
atgaagcagc tgcagcccg cctgcagacc ggcaccgagg agctgcgag cctgtacaac 240
accgtggcca cctgtactg cgtgcacgcc ggcacgagg tgcgcgacac caaggaggcc 300
ctggacaaga tcgaggagga gcagaacaag agccagcaga agaccagca ggccaaggag 360
gccgacggca aggtgagcca gaactacccc atcgtgcaga acctgcaggg ccagatgggtg 420
caccaggcca tcagcccccg caccctgaac gcctgggtga aggtgatcga ggagaaggcc 480
ttcagccccg aggtgatccc catgttcacc gccctgagcg agggcgccac ccccaggac 540
ctgaacacca tgctgaacac cgtgggcggc caccaggccg ccatgcagat gctgaaggac 600
accatcaacg aggaggccgc cgagtgggac cgctgcacc ccgtgcaggc cgccccctg 660
gcccccgccc agatgcgcga ccccgcggc agcgacatcg ccggcgccac cagcaccctg 720
caggagcaga tcgcctggat gaccagcaac cccccctgc ccgtgggcga catctacaag 780
cgctggatca tcctgggccc gaacaagatc gtgcgcatgt acagccccgt gagcatcctg 840
gacatccgcc agggccccaa ggagcccttc cgcgactacg tggaccgctt cttcaagacc 900
ctgcgcgcg agcaggccac ccaggacgtg aagaactgga tgaccgagac cctgctggtg 960
cagaacgcca acccgactg caagaccatc ctgcgcgccc tgggcccccg cgccaccctg 1020

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gaggagatga tgaccgcctg ccagggcggtg ggcgggccccg gccacaaggc ccgcgtgctg 1080
 gccgaggcca tgagccaggc caacagcggtg aacatcatga tgcagaagag caacttcaag 1140
 ggcccccgcc gcaacgtgaa gtgcttcaac tgcggcaagg agggccacat cgccaagaac 1200
 tgccgcgccc cccgcaagaa gggctgctgg aagtgcggca aggagggcca ccagatgaag 1260
 gactgcaccg agcgccaggc caacttcctg ggcaagatct ggcccagcca caagggccgc 1320
 cccggcaact tcctgcagaa ccgcagcgag cccgcccggc ccaccgtgcc caccgcccc 1380
 cccgcccgaga gcttccgctt cgaggagacc acccccggc ccaagcagga gcccaggac 1440
 cgcgagccct accgcgagcc cctgaccgcc ctgcgcagcc tgttcggcag cggccccctg 1500
 agccagtaa 1509

<210> 22

<211> 502

<212> PRT

<213> Human immunodeficiency virus

<400> 22

Met Gly Ala Arg Ala Ser Ile Leu Arg Gly Glu Lys Leu Asp Lys Trp
 1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys His Tyr Met Leu Lys
 20 25 30

His Leu Val Trp Ala Ser Arg Glu Leu Glu Gly Phe Ala Leu Asn Pro
 35 40 45

Gly Leu Leu Glu Thr Ala Glu Gly Cys Lys Gln Ile Met Lys Gln Leu
 50 55 60

Gln Pro Ala Leu Gln Thr Gly Thr Glu Glu Leu Arg Ser Leu Tyr Asn
 65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Ala Gly Ile Glu Val Arg Asp
 85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Gln
 100 105 110

Gln Lys Thr Gln Gln Ala Lys Glu Ala Asp Gly Lys Val Ser Gln Asn
 115 120 125

Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala Ile
 130 135 140

Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu Lys Ala
 145 150 155 160

Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu Gly Ala
 165 170 175

Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
 180 185 190

Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala Glu
 195 200 205

Trp Asp Arg Leu His Pro Val Gln Ala Gly Pro Val Ala Pro Gly Gln
210 215 220

Met Arg Asp Pro Arg Gly Ser Asp Ile Ala Gly Ala Thr Ser Thr Leu
225 230 235 240

Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Val Pro Val Gly
245 250 255

Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
260 265 270

Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
275 280 285

Pro Phe Arg Asp Tyr Val Asp Arg Phe Phe Lys Thr Leu Arg Ala Glu
290 295 300

Gln Ala Thr Gln Asp Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
305 310 315 320

Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Arg Ala Leu Gly Pro
325 330 335

Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
340 345 350

Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Ala Asn
355 360 365

Ser Val Asn Ile Met Met Gln Lys Ser Asn Phe Lys Gly Pro Arg Arg
370 375 380

Asn Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Lys Asn
385 390 395 400

Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
405 410 415

His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
420 425 430

Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Asn Arg
435 440 445

Ser Glu Pro Ala Ala Pro Thr Val Pro Thr Ala Pro Pro Ala Glu Ser
450 455 460

Phe Arg Phe Glu Glu Thr Thr Pro Ala Pro Lys Gln Glu Pro Lys Asp
465 470 475 480

Arg Glu Pro Tyr Arg Glu Pro Leu Thr Ala Leu Arg Ser Leu Phe Gly
485 490 495

Ser Gly Pro Leu Ser Gln
500

<210> 23
<211> 849
<212> PRT
<213> Human immunodeficiency virus

<400> 23
Met Arg Val Met Gly Ile Leu Lys Asn Tyr Gln Gln Trp Trp Met Trp
1 5 10 15
Gly Ile Leu Gly Phe Trp Met Leu Ile Ile Ser Ser Val Val Gly Asn
20 25 30
Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Lys
35 40 45
Thr Thr Leu Phe Cys Thr Ser Asp Ala Lys Ala Tyr Glu Thr Glu Val
50 55 60
His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
65 70 75 80
Gln Glu Ile Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys
85 90 95
Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
100 105 110
Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
115 120 125
Lys Cys Arg Asn Val Asn Ala Thr Asn Asn Ile Asn Ser Met Ile Asp
130 135 140
Asn Ser Asn Lys Gly Glu Met Lys Asn Cys Ser Phe Asn Val Thr Thr
145 150 155 160
Glu Leu Arg Asp Arg Lys Gln Glu Val His Ala Leu Phe Tyr Arg Leu
165 170 175
Asp Val Val Pro Leu Gln Gly Asn Asn Ser Asn Glu Tyr Arg Leu Ile
180 185 190
Asn Cys Asn Thr Ser Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe
195 200 205
Asp Pro Ile Pro Ile His Tyr Cys Thr Pro Ala Gly Tyr Ala Ile Leu
210 215 220
Lys Cys Asn Asn Gln Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val
225 230 235 240

Ser Ser Val Gln Cys Ala His Gly Ile Lys Pro Val Val Ser Thr Gln
 245 250 255
 Leu Leu Leu Asn Gly Ser Leu Ala Lys Gly Glu Ile Ile Ile Arg Ser
 260 265 270
 Glu Asn Leu Ala Asn Asn Ala Lys Ile Ile Ile Val Gln Leu Asn Lys
 275 280 285
 Pro Val Lys Ile Val Cys Val Arg Pro Asn Asn Asn Thr Arg Lys Ser
 290 295 300
 Val Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Glu Ile Ile
 305 310 315 320
 Gly Asp Ile Arg Gln Ala Tyr Cys Ile Ile Asn Lys Thr Glu Trp Asn
 325 330 335
 Ser Thr Leu Gln Gly Val Ser Lys Lys Leu Glu Glu His Phe Ser Lys
 340 345 350
 Lys Ala Ile Lys Phe Glu Pro Ser Ser Gly Gly Asp Leu Glu Ile Thr
 355 360 365
 Thr His Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asp Thr Ser
 370 375 380
 Gln Leu Phe Asn Ser Thr Tyr Ser Pro Ser Phe Asn Gly Thr Glu Asn
 385 390 395 400
 Lys Leu Asn Gly Thr Ile Thr Ile Thr Cys Arg Ile Lys Gln Ile Ile
 405 410 415
 Asn Met Trp Gln Lys Val Gly Arg Ala Met Tyr Ala Pro Pro Ile Ala
 420 425 430
 Gly Asn Leu Thr Cys Glu Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg
 435 440 445
 Asp Gly Gly Lys Thr Gly Pro Asn Asp Thr Glu Ile Phe Arg Pro Gly
 450 455 460
 Gly Gly Asp Met Arg Asp Asn Trp Arg Asn Glu Leu Tyr Lys Tyr Lys
 465 470 475 480
 Val Val Glu Ile Lys Pro Leu Gly Val Ala Pro Thr Glu Ala Lys Arg
 485 490 495
 Arg Val Val Glu Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Val Phe
 500 505 510
 Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Ile
 515 520 525

Thr Leu Thr Val Gln Ala Arg Leu Leu Leu Ser Gly Ile Val Gln Gln
530 535 540

Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln
545 550 555 560

Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Thr Arg Ile Leu Ala Val
565 570 575

Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser
580 585 590

Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ser Ser Trp Ser
595 600 605

Asn Arg Ser His Asp Glu Ile Trp Asp Asn Met Thr Trp Met Gln Trp
610 615 620

Asp Arg Glu Ile Asn Asn Tyr Thr Asp Thr Ile Tyr Arg Leu Leu Glu
625 630 635 640

Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Lys Asp Leu Leu Ala Leu
645 650 655

Asp Ser Trp Gln Asn Leu Trp Asn Trp Phe Ser Ile Thr Asn Trp Leu
660 665 670

Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu
675 680 685

Arg Ile Ile Phe Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly
690 695 700

Tyr Ser Pro Leu Pro Phe Gln Thr Leu Thr Pro Asn Pro Arg Glu Pro
705 710 715 720

Asp Arg Leu Gly Arg Ile Glu Glu Glu Gly Gly Glu Gln Asp Arg Gly
725 730 735

Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ala Leu Ala Trp Asp Asp
740 745 750

Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Phe Ile
755 760 765

Leu Ile Ala Ala Arg Val Leu Glu Leu Leu Gly Gln Arg Gly Trp Glu
770 775 780

Ala Leu Lys Tyr Leu Gly Ser Leu Val Gln Tyr Trp Gly Leu Glu Leu
785 790 795 800

Lys Lys Ser Ala Ile Ser Leu Leu Asp Thr Ile Ala Ile Ala Val Ala
805 810 815

Glu Gly Thr Asp Arg Ile Ile Glu Phe Ile Gln Arg Ile Cys Arg Ala
820 825 830

Ile Arg Asn Ile Pro Arg Arg Ile Arg Gln Gly Phe Glu Ala Ala Leu
835 840 845

Gln

<210> 24

<211> 855

<212> PRT

<213> Human immunodeficiency virus

<400> 24

Met Arg Val Arg Gly Ile Leu Arg Ser Trp Gln Gln Trp Trp Ile Trp
1 5 10 15

Gly Ile Leu Gly Phe Trp Ile Cys Ser Gly Leu Gly Asn Leu Trp Val
20 25 30

Thr Val Tyr Asp Gly Val Pro Val Trp Arg Glu Ala Ser Thr Thr Leu
35 40 45

Phe Cys Ala Ser Asp Ala Lys Ala Tyr Glu Lys Glu Val His Asn Val
50 55 60

Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile
65 70 75 80

Glu Leu Asp Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asp Met
85 90 95

Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
100 105 110

Lys Pro Arg Val Lys Leu Thr Pro Leu Cys Val Thr Leu Lys Cys Thr
115 120 125

Asn Tyr Ser Thr Asn Tyr Ser Asn Thr Met Asn Ala Thr Ser Tyr Asn
130 135 140

Asn Asn Thr Thr Glu Glu Ile Lys Asn Cys Thr Phe Asn Met Thr Thr
145 150 155 160

Glu Leu Arg Asp Lys Lys Gln Gln Val Tyr Ala Leu Phe Tyr Lys Leu
165 170 175

Asp Ile Val Pro Leu Asn Ser Asn Ser Ser Glu Tyr Arg Leu Ile Asn
180 185 190

Cys Asn Thr Ser Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Asp
195 200 205

Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys
 210 215 220
 Cys Lys Asn Asn Thr Ser Asn Gly Thr Gly Pro Cys Gln Asn Val Ser
 225 230 235 240
 Thr Val Gln Cys Thr His Gly Ile Lys Pro Val Val Ser Thr Pro Leu
 245 250 255
 Leu Leu Asn Gly Ser Leu Ala Glu Gly Gly Glu Ile Ile Ile Arg Ser
 260 265 270
 Lys Asn Leu Ser Asn Asn Ala Tyr Thr Ile Ile Val His Leu Asn Asp
 275 280 285
 Ser Val Glu Ile Val Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly
 290 295 300
 Ile Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Glu Asn Ile Ile
 305 310 315 320
 Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Ala Gly Glu Trp Asn
 325 330 335
 Lys Ala Val Gln Arg Val Ser Ala Lys Leu Arg Glu His Phe Pro Asn
 340 345 350
 Lys Thr Ile Glu Phe Gln Pro Ser Ser Gly Gly Asp Leu Glu Ile Thr
 355 360 365
 Thr His Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asn Thr Ser
 370 375 380
 Lys Leu Phe Asn Ser Ser Tyr Asn Gly Thr Ser Tyr Arg Gly Thr Glu
 385 390 395 400
 Ser Asn Ser Ser Ile Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile
 405 410 415
 Asp Met Trp Gln Lys Val Gly Arg Ala Ile Tyr Ala Pro Pro Ile Glu
 420 425 430
 Gly Asn Ile Thr Cys Ser Ser Ser Ile Thr Gly Leu Leu Leu Ala Arg
 435 440 445
 Asp Gly Gly Leu Asp Asn Ile Thr Thr Glu Ile Phe Arg Pro Gln Gly
 450 455 460
 Gly Asp Met Lys Asp Asn Trp Arg Asn Glu Leu Tyr Lys Tyr Lys Val
 465 470 475 480
 Val Glu Ile Lys Pro Leu Gly Val Ala Pro Thr Glu Ala Lys Arg Arg
 485 490 495

Val Val Glu Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Val Ile Phe
 500 505 510
 Gly Phe Leu Gly Ala Ala Gly Ser Asn Met Gly Ala Ala Ser Ile Thr
 515 520 525
 Leu Thr Ala Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln
 530 535 540
 Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Met Leu Gln Leu
 545 550 555 560
 Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Val Leu Ala Ile Glu
 565 570 575
 Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly
 580 585 590
 Lys Leu Ile Cys Thr Thr Thr Val Pro Trp Asn Ser Ser Trp Ser Asn
 595 600 605
 Lys Thr Gln Gly Glu Ile Trp Glu Asn Met Thr Trp Met Gln Trp Asp
 610 615 620
 Lys Glu Ile Ser Asn Tyr Thr Gly Ile Ile Tyr Arg Leu Leu Glu Glu
 625 630 635 640
 Ser Gln Asn Gln Gln Glu Gln Asn Glu Lys Asp Leu Leu Ala Leu Asp
 645 650 655
 Ser Arg Asn Asn Leu Trp Ser Trp Phe Asn Ile Ser Asn Trp Leu Trp
 660 665 670
 Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg
 675 680 685
 Ile Ile Phe Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr
 690 695 700
 Ser Pro Leu Ser Phe Gln Thr Leu Thr Pro Asn Pro Arg Gly Leu Asp
 705 710 715 720
 Arg Leu Gly Arg Ile Glu Glu Glu Gly Gly Glu Gln Asp Arg Asp Arg
 725 730 735
 Ser Ile Arg Leu Val Gln Gly Phe Leu Ala Leu Ala Trp Asp Asp Leu
 740 745 750
 Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Ile Leu
 755 760 765
 Val Thr Ala Arg Val Val Glu Leu Leu Gly Arg Ser Ser Pro Arg Gly
 770 775 780

Leu Gln Arg Gly Trp Glu Ala Leu Lys Tyr Leu Gly Ser Leu Val Gln
785 790 795 800

Tyr Trp Gly Leu Glu Leu Lys Lys Ser Ala Thr Ser Leu Leu Asp Ser
805 810 815

Ile Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Ile Ile Glu Val Ile
820 825 830

Gln Arg Ile Tyr Arg Ala Phe Cys Asn Ile Pro Arg Arg Val Arg Gln
835 840 845

Gly Phe Glu Ala Ala Leu Gln
850 855

<210> 25

<211> 20

<212> PRT

<213> Human immunodeficiency virus

<400> 25

Asp Ile Lys Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg
1 5 10 15

Phe Phe Lys Thr
20

<210> 26

<211> 60

<212> DNA

<213> Human immunodeficiency virus

<400> 26

gacataaaac aaggaccaa agagcccttt agagactatg tagaccggtt ctttaaaacc 60

<210> 27

<211> 20

<212> PRT

<213> Human immunodeficiency virus

<400> 27

Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg
1 5 10 15

Phe Phe Lys Thr
20

<210> 28

<211> 47

<212> PRT

<213> Human immunodeficiency virus

<400> 28

Thr Ile Thr Ile Thr Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln
1 5 10 15

Lys Val Gly Arg Ala Met Tyr Ala Pro Pro Ile Ala Gly Asn Leu Thr
20 25 30

Cys Glu Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
35 40 45

<210> 29

<211> 48

<212> PRT

<213> Human immunodeficiency virus

<400> 29

Ser Ile Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asp Met Trp
1 5 10 15

Gln Lys Val Gly Arg Ala Ile Tyr Ala Pro Pro Ile Glu Gly Asn Ile
20 25 30

Thr Cys Ser Ser Ser Ile Thr Gly Leu Leu Leu Ala Arg Asp Gly Gly
35 40 45

<210> 30

<211> 2469

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PR975(+)

<400> 30

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ggccaccaga tgaaggactg caccgagcgc caggccaact tcttcgcga ggacctggcc 240
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agccgcgagc tgcaggtgcg cggcgacaac ccccgagcg aggcggcgc cgagcgccag 360
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gtgcgccagt acgaccagat cctgatcgag atctgcggca agaaggccat cggcaccgtg 600
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gagatcgtga	tctaccagta	catggacgac	ctgtacgtgg	gcagcgacct	ggagatcggc	1260
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cccgacaaga	agcaccagaa	ggagcccccc	ttcctgtgga	tgggctacga	gctgcacccc	1380
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ggtgaattc						2469

<210> 31

<211> 2463

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PR975YM

<400> 31

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cacatcgccc	gcaactgccg	cgccccccgc	aagaagggtc	gctggaagtg	cggcaaggag	180
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agccgcgagc	tgcaggtgcg	cggcgacaac	ccccgcagcg	aggccggcgc	cgagcgccag	360
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ggcgcccgaga	tcaaggaggc	cctgctggac	accggcgccg	acgacaccgt	gctggaggag	480
atgagcctgc	ccggcaagtg	gaagcccaag	atgatcgccg	gcatacgccg	cttcatcaag	540
gtgcgccagt	acgaccagat	cctgatcgag	atctgcggca	agaaggccat	cggcaccgtg	600
ctgatcgggc	ccacccccgt	gaacatcatc	ggcgcaaca	tgctgacca	gctgggctgc	660
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cccgcggggc	tgaagaagaa	gaagagcgtg	accgtgctgg	acgtgggcga	cgctacttcc	1020
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 ttc 2463

<210> 32

<211> 2457

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PR975YMWM

<400> 32

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<210> 33

<211> 9781

<212> DNA

<213> Human immunodeficiency virus

<400> 33

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tgaccttttg	atggtgctac	aagctagtgc	cagttgaccc	aggggaggtg	gaagaggcca	180
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